##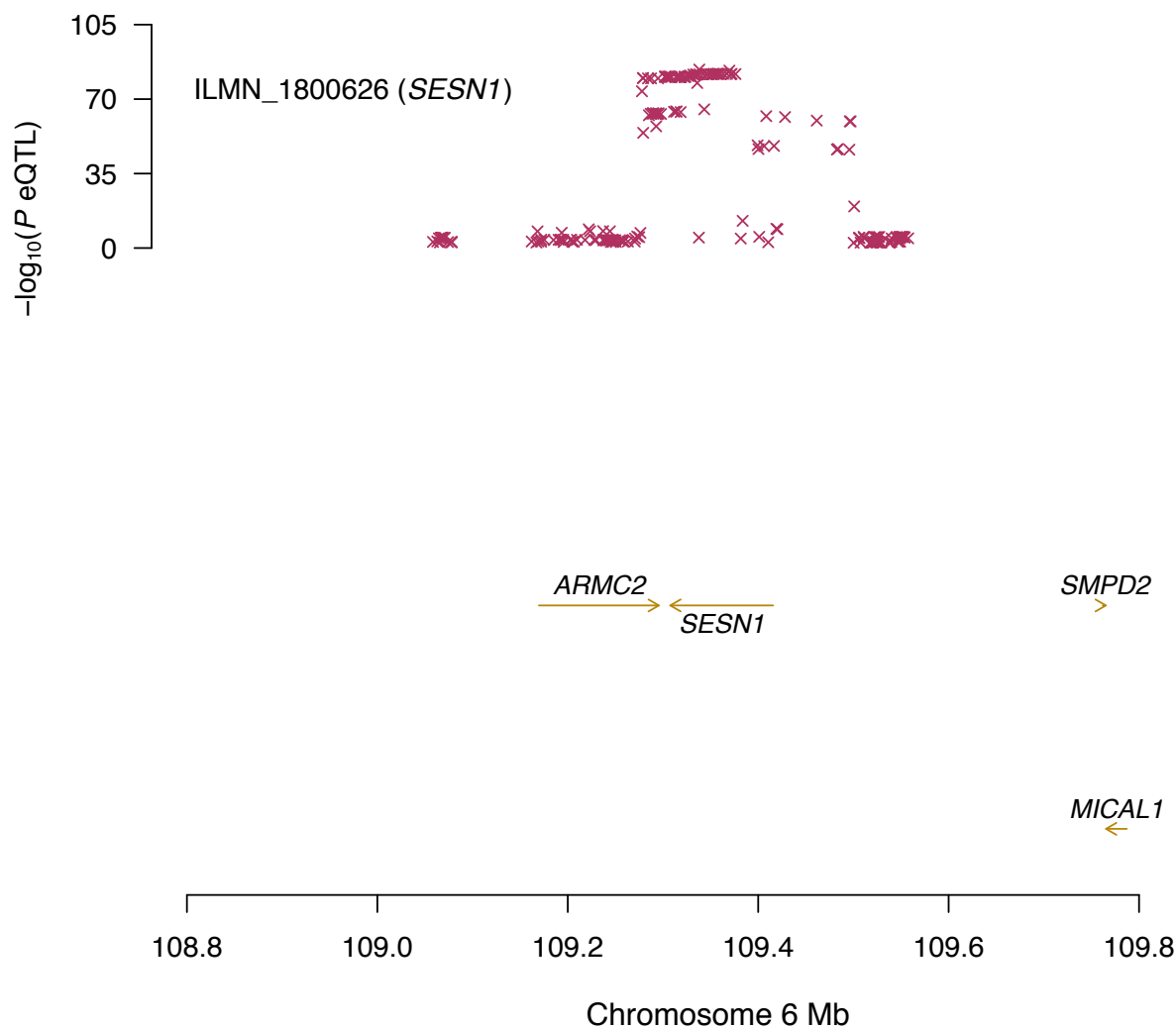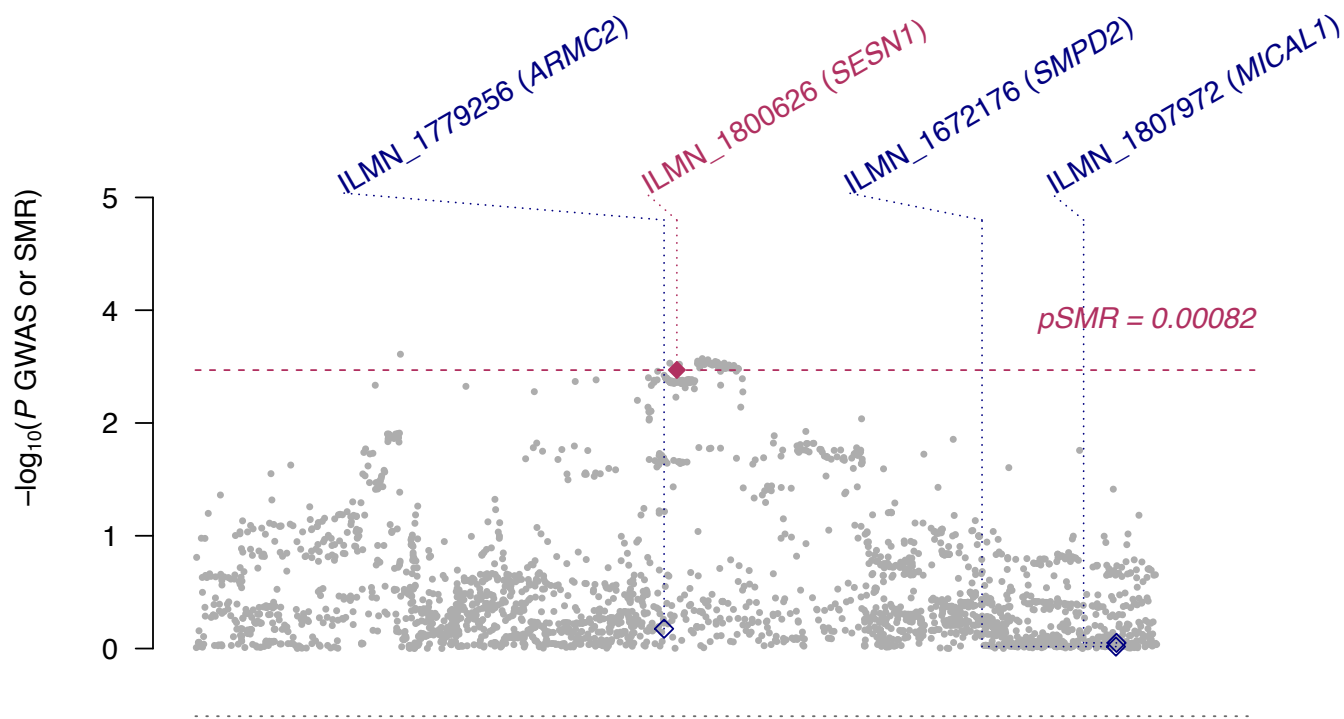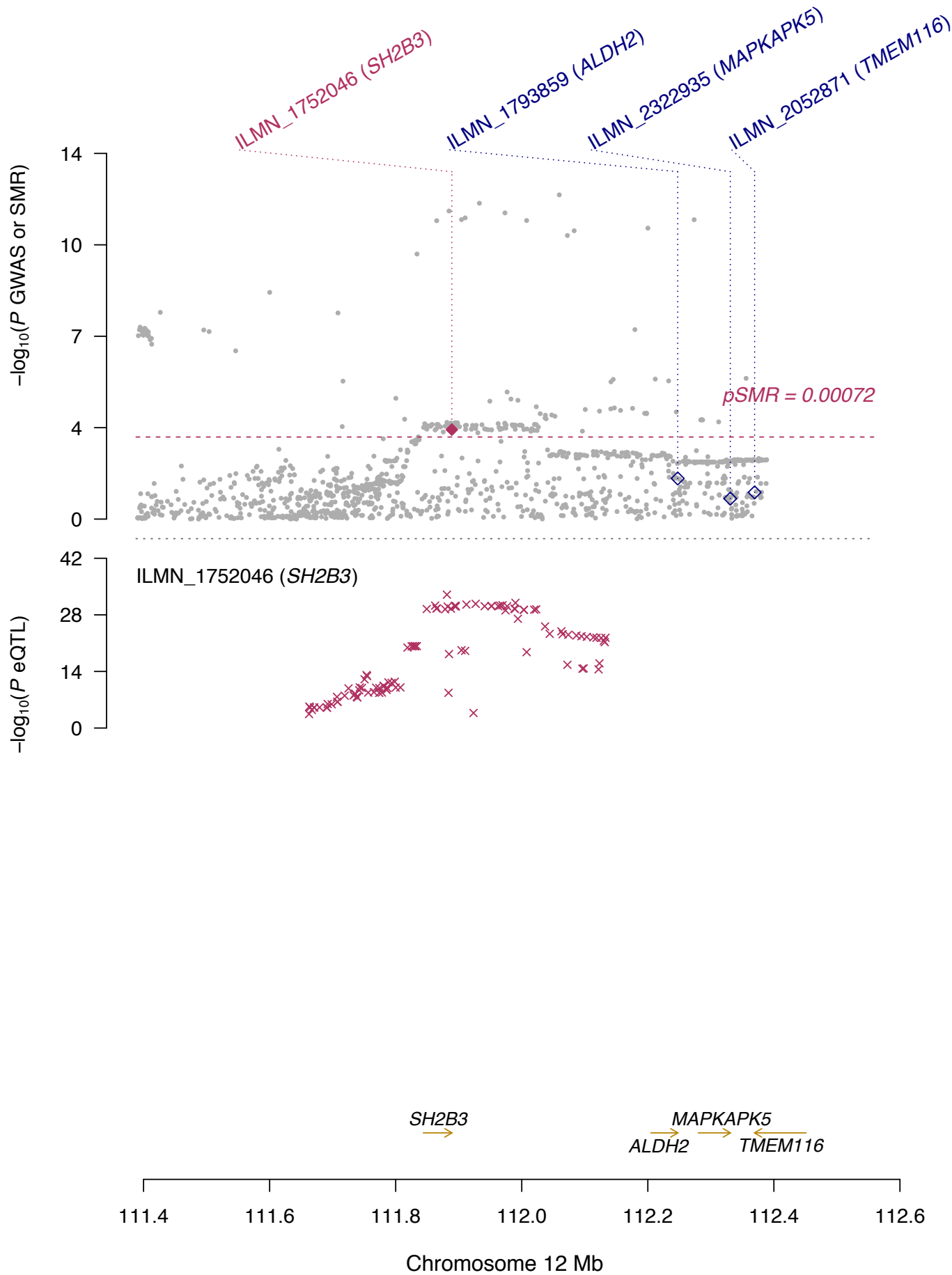 Supplementary file 1: Loci with significantly predicted candidate genes using SMR-HEIDI test and two eQTL datasets (blood tissue)

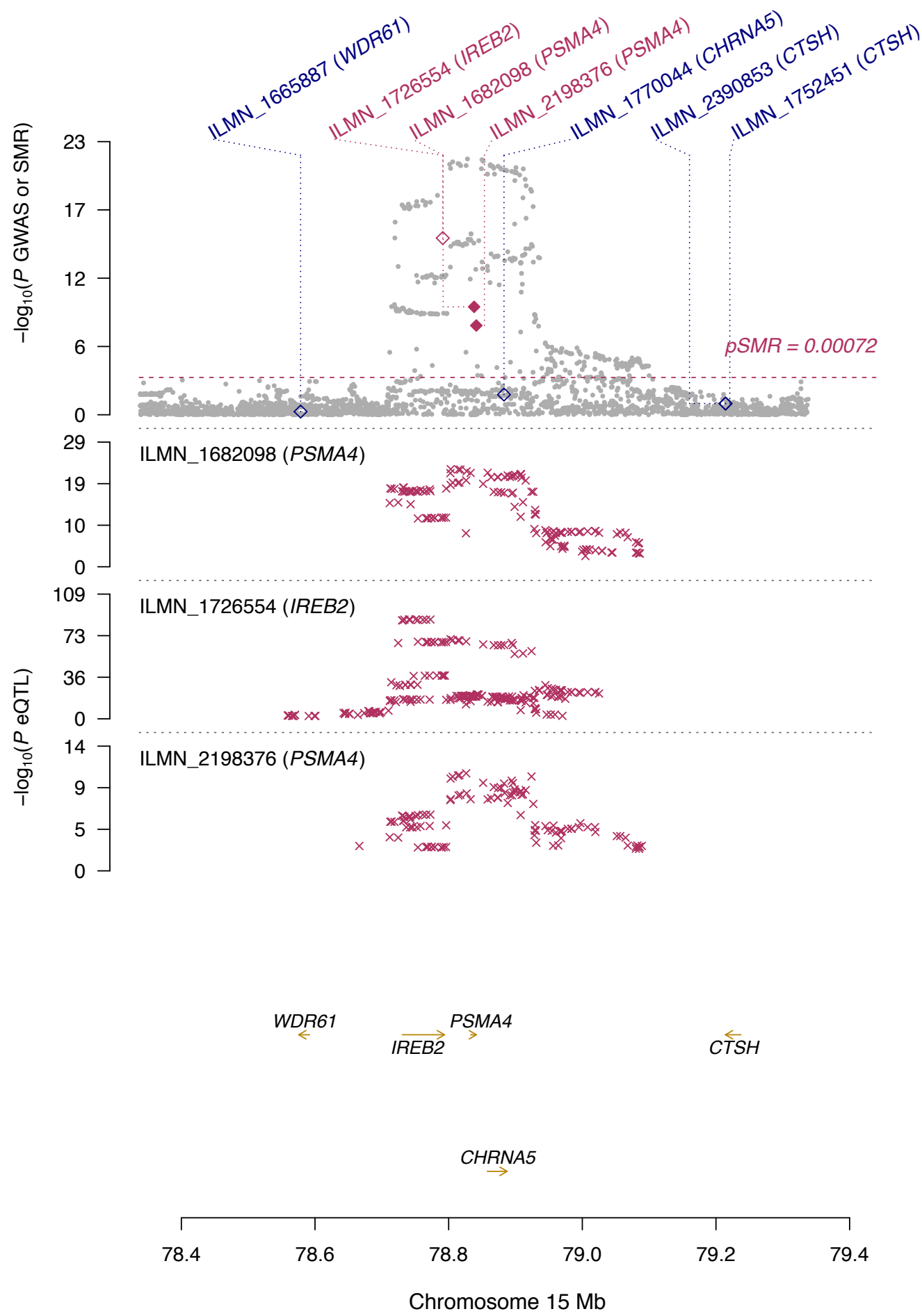| At or near	rsID	Chr	Position	SMR Genes	Westra		CAGE	
					P SMR	P HEIDI	P SMR	P HEIDI
CELSR2/PSRC1	rs4970836	1	109821797	PSRC1			7.3E-08	0.2980
FOXO3	rs3800231	6	108998266	SESN1	8.2E-04	0.2640		
ATXN2/BRAP	rs11065979	12	112059557	SH2B3	3.8E-04	0.0602		
CHRNA3/5	rs8042849	15	78817929	PSMA4	8.2E-10	0.2240	1.3E-05	0.1080
CHRNA3/5	rs8042849	15	78817929	PSMA4	3.1E-08	0.5590		
FURIN/FES	rs6224	15	91423543	FES	1.8E-06	0.0550		
FURIN/FES	rs6224	15	91423543	FURIN			1.8E-04	0.0621
LDLR	rs142158911	19	11190534	KANK2	7.2E-04	0.5660		

All 24 loci discovered or replicated in our study were tested against blood tissue eQTL data from two studies, Westra and CAGE. Only genes that pass FDR < 5% threshold for the SMR test and P > 0.05 threshold for HEIDI test are listed for their corresponding loci. At or near – nearby gene or cluster of genes to lead variant; rsID – reference SNP cluster ID for the index SNP in the region; Chr – chromosome Position – Base-pair position on chromosome (build GRCh37); SMR genes – genes prioritised by SMR within the given locus.
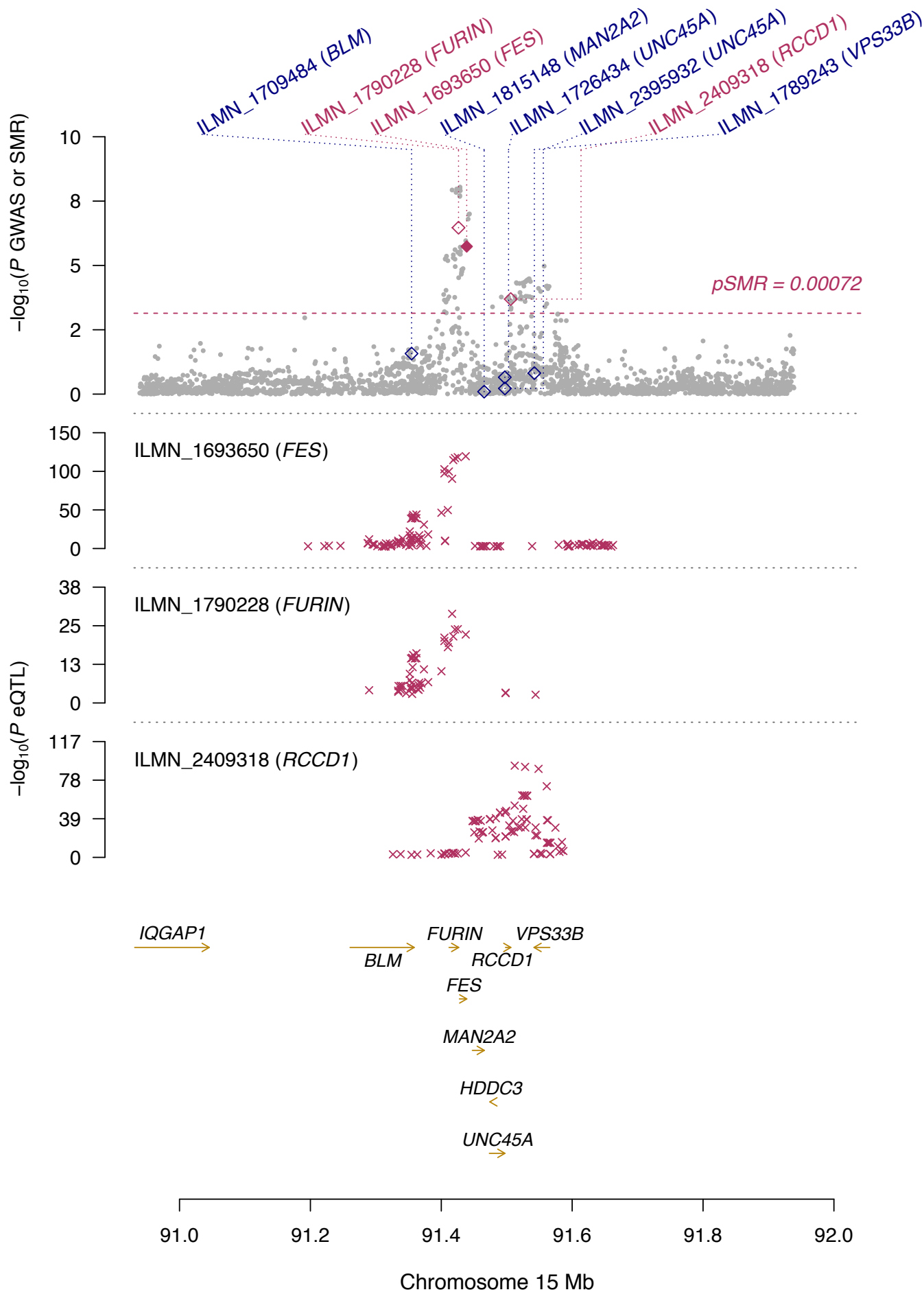
The following pages contain plots of the lifespan GWAS and eQTL signals. Gene expression probe names are provided with the corresponding gene names in brackets. The pSMR threshold corresponds to a significance level of FDR < 5%, and the gene expression probes that have SMR signal passing this threshold are displayed as red diamonds, otherwise blue. Filled diamonds indicate that the corresponding probes also pass the P > 0.05 threshold for the HEIDI test, i.e. the expressions of the particular genes possibly share causal variants with the lifespan GWAS signals.
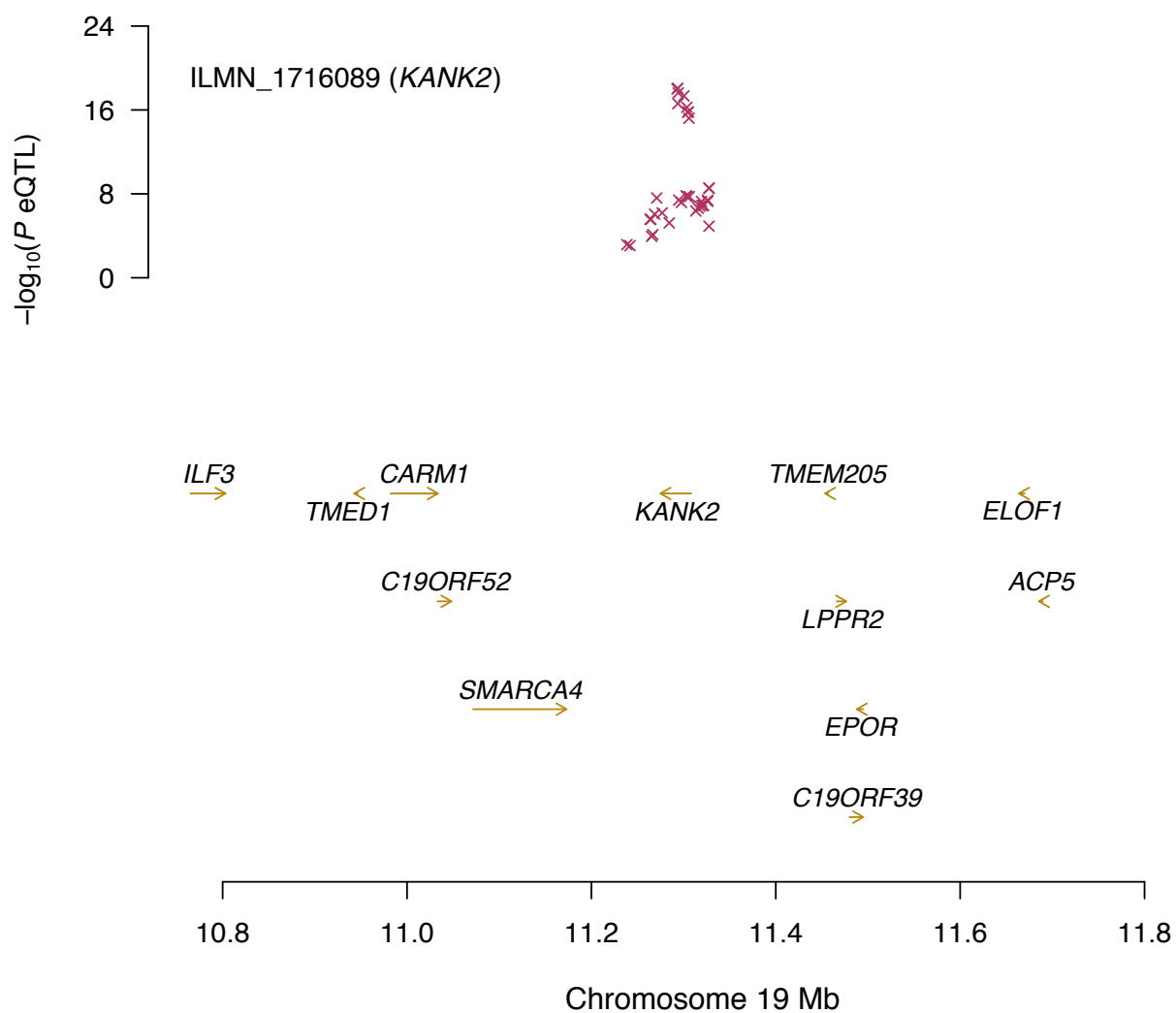
Westra

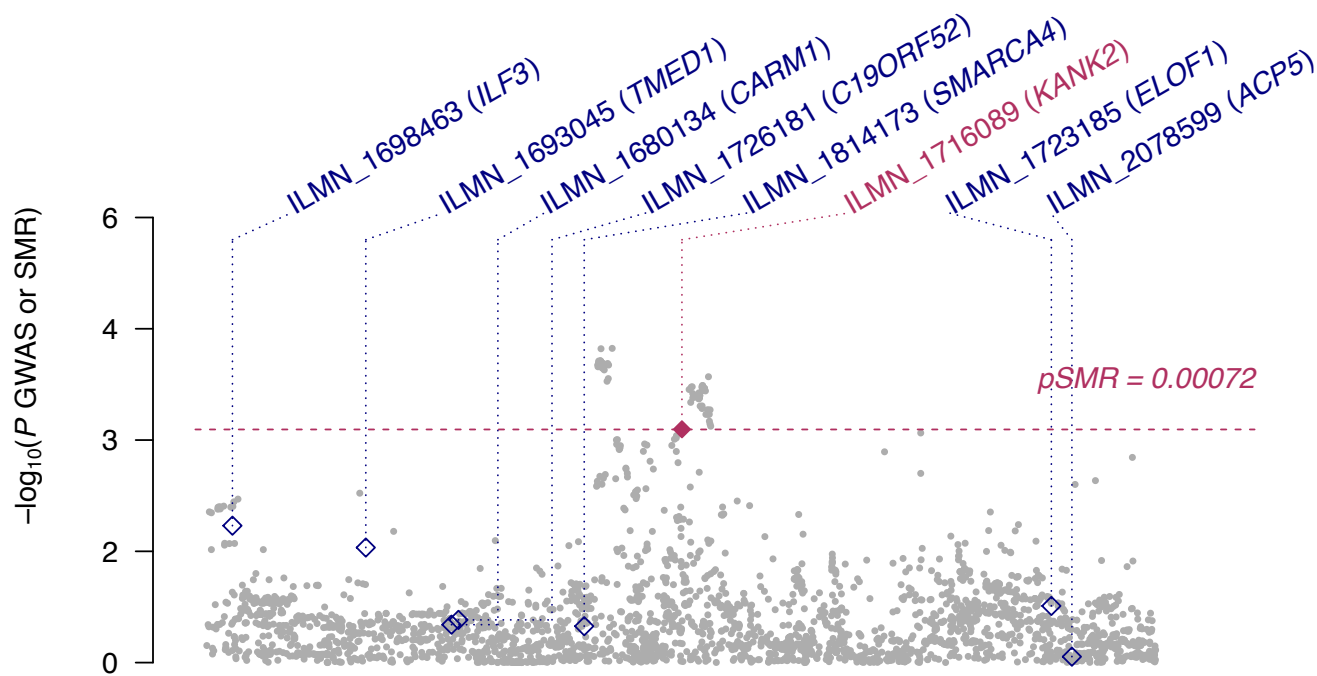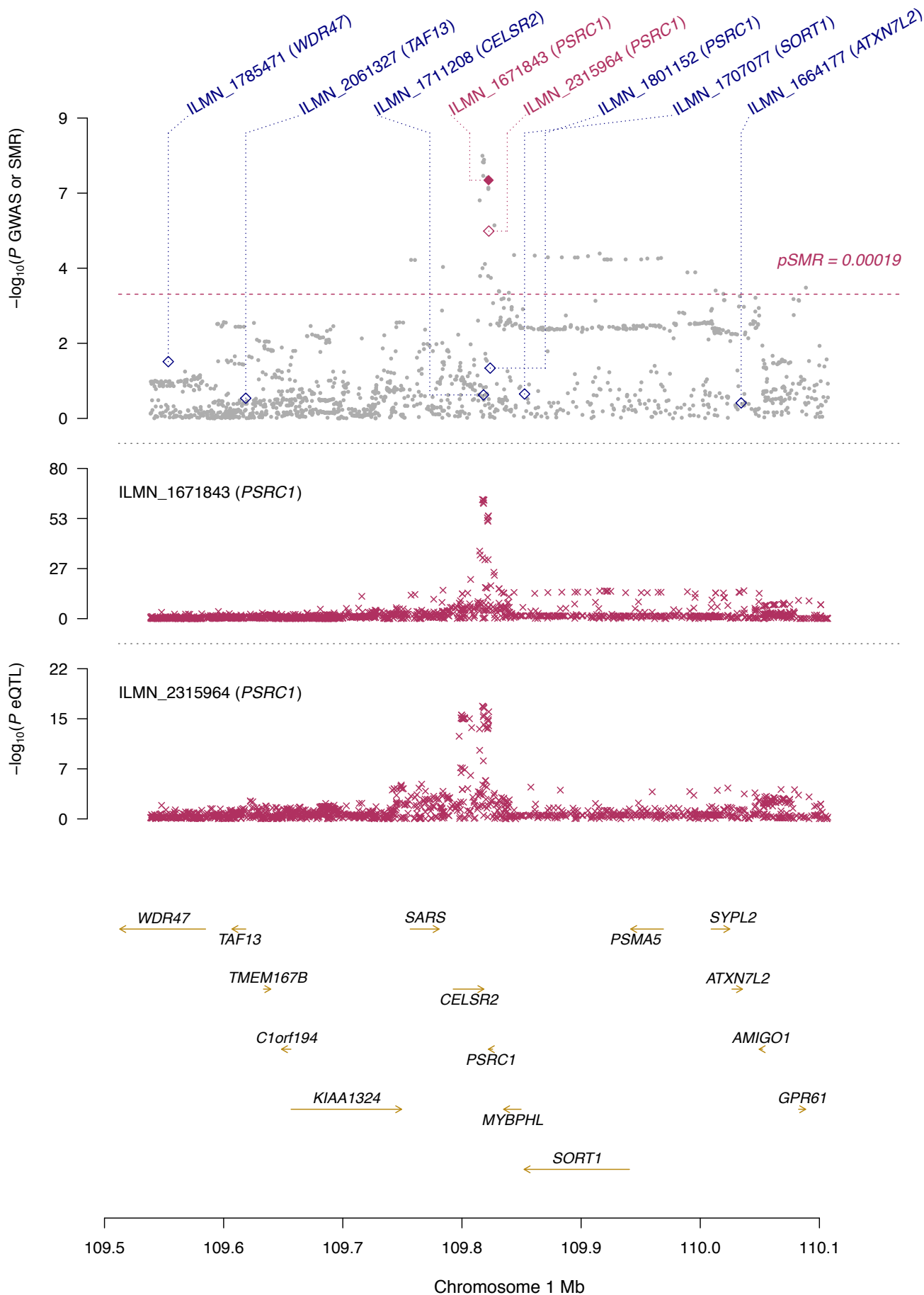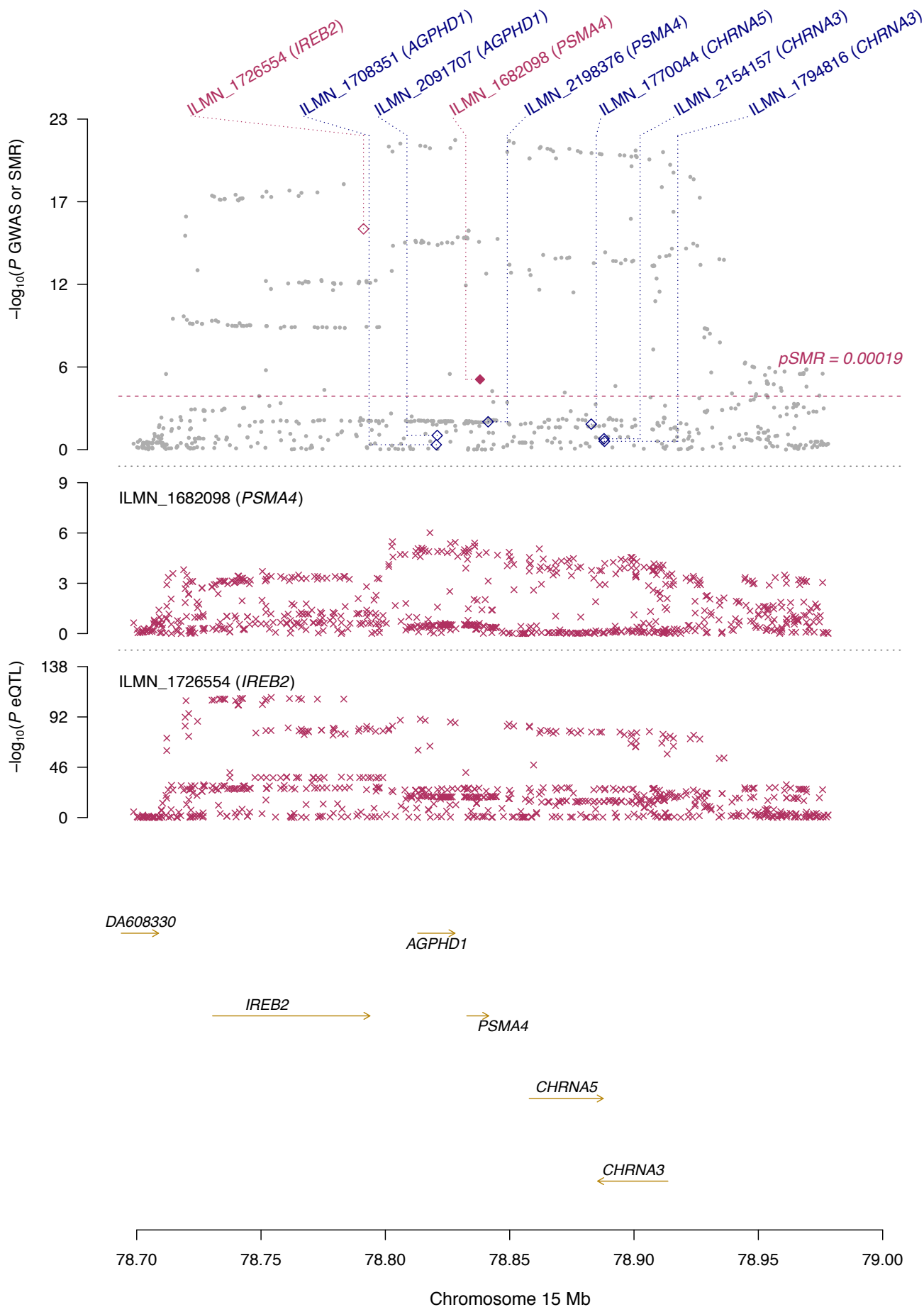$-\log_{10}(P \text{ GWAS or SMR})$

ILMN_1752046 (SH2B3)
ILMN_1793859 (ALDH2)
ILMN_2322935 (MAPKAPK5)
ILMN_2052871 (TMEM116)

pSMR = 0.00072

ILMN_1752046 (SH2B3)

$-\log_{10}(P \text{ eQTL})$

SH2B3
MAPKAPK5
ALDH2
TMEM116

Chromosome 12 Mb

Westra

Westra

Westra

ILMN_1698463 (*ILF3*)
ILMN_1693045 (*TMED1*)
ILMN_1680134 (*CARM1*)
ILMN_1726181 (*C19ORF52*)
ILMN_1814173 (*SMARCA4*)
ILMN_1716089 (*KANK2*)
ILMN_1723185 (*ELOF1*)
ILMN_2078599 (*ACP5*)

$-\log_{10}(P$ GWAS or SMR)

pSMR = 0.00072

$-\log_{10}(P$ eQTL)

ILMN_1716089 (*KANK2*)

ILF3
CARM1
TMED1
TMEM205
KANK2
ELOF1
C19ORF52
ACP5
LPPR2
SMARCA4
EPOR
C19ORF39

Chromosome 19 Mb

CAGE

CAGE

CAGE